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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=5; day=3; hr=10; min=10; sec=43; ms=829;]

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Application No: 10590870

Version No: 1.0

Input Set:

Output Set:

Started: 2010-04-23 14:53:05.942

Finished: 2010-04-23 14:53:09.612

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 670 ms

Total Warnings: 51

Total Errors: 2

No. of SeqIDs Defined: 51

Actual SeqID Count: 51

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (1) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (17) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (18) |

Input Set:

Output Set:

Started: 2010-04-23 14:53:05.942
Finished: 2010-04-23 14:53:09.612
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 670 ms
Total Warnings: 51
Total Errors: 2
No. of SeqIDs Defined: 51
Actual SeqID Count: 51

| Error code | Error Description |
|------------|--|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (19) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed |

SEQUENCE LISTING

<110> Fox, Judith A.
Harding, Fiona A.
Rashid, M. Harunur
Schellenberger, Volker

<120> CAB Molecules

<130> GC839-US

<140> 10590870

<141> 2010-04-23

<150> PCT/US05/12270

<151> 2005-04-12

<150> US 60/562,386

<151> 2004-04-15

<150> US 60/636,002

<151> 2004-12-14

<160> 51

<170> PatentIn version 3.2

 $\langle 210 \rangle$ 1

<211> 262

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> engineered T84.66 antibody

 $\langle 400 \rangle$ 1

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly

1 5 10 15

Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe

20 25 30

Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro

35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val

50 55 60

Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp

65 70 75 80

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn

85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly

100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

| | | |
|-----|-----|-----|
| 115 | 120 | 125 |
|-----|-----|-----|

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

130 135 140

Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 | | 150 | | 155 | | 160 | | | | | | | | | |
| Leu | Ser | Cys | Thr | Ala | Ser | Gly | Phe | Asn | Ile | Lys | Asp | Thr | Tyr | Met | His |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Trp | Val | Lys | Gln | Arg | Pro | Glu | Gln | Gly | Leu | Glu | Trp | Ile | Gly | Arg | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asp | Pro | Ala | Asn | Gly | Asn | Ser | Lys | Tyr | Val | Pro | Lys | Phe | Gln | Gly | Lys |
| | | 195 | | | | 200 | | | | | 205 | | | | |
| Ala | Thr | Ile | Thr | Ala | Asp | Thr | Ser | Ser | Asn | Thr | Ala | Tyr | Leu | Gln | Leu |
| | 210 | | | | | 215 | | | | 220 | | | | | |
| Thr | Ser | Leu | Thr | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala | Pro | Phe |
| 225 | | | | | 230 | | | | 235 | | | | | 240 | |
| Gly | Tyr | Tyr | Val | Ser | Asp | Tyr | Ala | Met | Ala | Tyr | Trp | Gly | Gln | Gly | Thr |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Ser | Val | Thr | Val | Ser | Ser | | | | | | | | | | |
| | | | 260 | | | | | | | | | | | | |

<210> 2
 <211> 623
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAB 1.10 construct

<400> 2

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Ser | Leu | Ala | Val | Ser | Leu | Gly |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Gln | Arg | Ala | Thr | Met | Ser | Cys | Arg | Ala | Gly | Glu | Ser | Val | Asp | Ile | Phe |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Gly | Val | Gly | Phe | Leu | His | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Pro | Pro |
| | 35 | | | | 40 | | | | | 45 | | | | | |
| Lys | Leu | Leu | Ile | Tyr | Arg | Ala | Ser | Asn | Leu | Glu | Ser | Gly | Ile | Pro | Val |
| | 50 | | | | 55 | | | | 60 | | | | | | |
| Arg | Phe | Ser | Gly | Thr | Gly | Ser | Arg | Thr | Asp | Phe | Thr | Leu | Ile | Ile | Asp |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Pro | Val | Glu | Ala | Asp | Asp | Val | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Thr | Asn |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Glu | Asp | Pro | Tyr | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Gly |
| | 100 | | | | | | 105 | | | | | | 110 | | |
| Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly |
| | 115 | | | | 120 | | | | | | | 125 | | | |
| Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Glu | Val | Gln |
| | 130 | | | | 135 | | | | | | 140 | | | | |
| Leu | Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val | Glu | Pro | Gly | Ala | Ser | Val | Lys |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Leu | Ser | Cys | Thr | Ala | Ser | Gly | Phe | Asn | Ile | Lys | Asp | Thr | Tyr | Met | His |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Trp | Val | Lys | Gln | Arg | Pro | Glu | Gln | Gly | Leu | Glu | Trp | Ile | Gly | Arg | Ile |
| | 180 | | | | | | | 185 | | | | | 190 | | |
| Asp | Pro | Ala | Asn | Gly | Asn | Ser | Lys | Tyr | Val | Pro | Lys | Phe | Gln | Gly | Lys |
| | 195 | | | | | 200 | | | | | 205 | | | | |
| Ala | Thr | Ile | Thr | Ala | Asp | Thr | Ser | Ser | Asn | Thr | Ala | Tyr | Leu | Gln | Leu |
| | 210 | | | | | 215 | | | | 220 | | | | | |
| Thr | Ser | Leu | Thr | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala | Pro | Phe |
| 225 | | | | | 230 | | | | 235 | | | | | 240 | |
| Gly | Tyr | Tyr | Val | Ser | Asp | Tyr | Ala | Met | Ala | Tyr | Trp | Gly | Gln | Gly | Thr |
| | | | 245 | | | | | 250 | | | | | 255 | | |

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| gacatcgccc | tgacccagag | cccggcaagc | ctggctgttt | ccctgggcca | gcgtgccact | 60 |
| atgtcctgca | gagcgggtga | gtctgttgac | attttcggtg | tcggttttct | gcactggtac | 120 |
| caacagaaac | cgggtcagcc | gccaaaactg | ctgatctatc | gtgcttctaa | cctggagtc | 180 |
| ggcatcccgg | tacgtttctc | cgggtactggc | tctcgtactg | attttaccct | gattatcgac | 240 |
| cgggtggaag | cagacgatgt | tgccacctac | tattgccagc | agaccaacga | ggatccgtac | 300 |
| accttcggtg | gcggtactaa | actggagatc | aaaggcgggtg | gtggttctgg | tgggtggtgt | 360 |
| agcggcggcg | gtggtagcgg | tggcgggtggc | agcgggtggtg | gtggctctgg | tggcgggtggc | 420 |
| tctgaagtgc | agctgcagca | gtccgggtgcg | gagctcggtg | aaccgggcgc | ttctgtgaaa | 480 |
| ctgtcttgca | ctgcatctgg | tttcaacatt | aaggacacct | acatgcactg | ggtgaaacaa | 540 |
| cgcgcggaac | aggggtctgga | gtggatcggg | cgcacgcgac | cggctaaccg | taacagcaaa | 600 |
| tacgtgccaa | aattccaggg | taaagcaacc | atcactgctg | atacctctc | taacactgct | 660 |
| tacctgcagc | tgacttccct | gactagcgaa | gacaccgcgg | tttattactg | cgctccgttc | 720 |
| ggctactatg | tcagcgatta | cgcaatggcc | tactggggtc | agggcacctc | tgttaccgtt | 780 |
| tctagc | | | | | | 786 |

<210> 4

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> CAB 1.10 construct

<400> 4

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|-------------|-------------|-------------|-------------|------------|-------------|------|
| gacatcgccc | tgacccagag | cccggcaagc | ctggctgttt | ccctgggcca | gcgtgccact | 60 |
| atgtcctgca | gagcgggtga | gtctgttgac | attttcggtg | tcggttttct | gcactggtac | 120 |
| caacagaaac | cgggtcagcc | gccaaaactg | ctgatctatc | gtgcttctaa | cctggagtc | 180 |
| ggcatcccgg | tacgtttctc | cgggtactggc | tctcgtactg | attttaccct | gattatcgac | 240 |
| cgggtggaag | cagacgatgt | tgccacctac | tattgccagc | agaccaacga | ggatccgtac | 300 |
| accttcggtg | gcggtactaa | actggagatc | aaaggcgggtg | gtggttctgg | tgggtggtgt | 360 |
| agcggcggcg | gtggtagcgg | tggcgggtggc | agcgggtggtg | gtggctctgg | tggcgggtggc | 420 |
| tctgaagtgc | agctgcagca | gtccgggtgcg | gagctcggtg | aaccgggcgc | ttctgtgaaa | 480 |
| ctgtcttgca | ctgcatctgg | tttcaacatt | aaggacacct | acatgcactg | ggtgaaacaa | 540 |
| cgcgcggaac | aggggtctgga | gtggatcggg | cgcacgcgac | cggctaaccg | taacagcaaa | 600 |
| tacgtgccaa | aattccaggg | taaagcaacc | atcactgctg | atacctctc | taacactgct | 660 |
| tacctgcagc | tgacttccct | gactagcgaa | gacaccgcgg | tttattactg | cgctccgttc | 720 |
| ggctactatg | tcagcgatta | cgcaatggcc | tactggggtc | agggcacctc | tgttaccgtt | 780 |
| tctagcacac | cgggtgtcaga | aaaacagctg | gcggaggtgg | tcgcgaatac | gattaccccg | 840 |
| ctgatgaaag | cccagtctgt | tccaggcatg | gcggtggccg | ttatttatca | gggaaaaccg | 900 |
| cactattaca | catttggtcaa | ggccgatatc | gcggcgaata | aacccggtac | gcctcagacc | 960 |
| ctgttcgagc | tgggttctat | aagtaaaacc | ttcacccggc | ttttaggtgg | ggatgccatt | 1020 |
| gctcgcgggtg | aaatttcgct | ggacgatgcg | gtgaccagat | actggccaca | gctgacgggc | 1080 |
| aagcagtggc | aggggtattcg | tatgctggat | ctcgccacct | acaccgctgg | cggcctgccg | 1140 |
| ctacagggtac | cggatgaggt | cacggataac | gcctccctgc | tgcgctttta | tcaaaaactgg | 1200 |
| cagccgcagt | ggaagcctgg | cacaacgcgt | ctttacgcca | acgccagcat | cggctctttt | 1260 |
| ggtgcgctgg | cgggtcaaacc | ttctggcatg | ccctatgagc | aggccatgac | gacgcgggtc | 1320 |
| cttaagccgc | tcaagctgga | ccatacctgg | attaacgtgc | cgaagcgga | agaggcgcat | 1380 |
| tacgcctggg | gctatcgtga | cggtaaagcg | gtgcgcgttt | cgccgggtat | gctggatgca | 1440 |
| caagcctatg | gcgtgaaaac | caacgtgcag | gatatggcga | actgggtcat | ggcaaacatg | 1500 |
| gcgcgcggaga | acgttgctga | tgcctcactt | aagcagggca | tcgcgctggc | gcagtcgcgc | 1560 |
| tactggcgta | tcgggtcaat | gtatcagggg | ctgggctggg | agatgctcaa | ctggcccgtg | 1620 |
| gaggccaaca | cgggtggtcga | gacgagtttt | ggtaatgtag | cactggcgcc | gttgcccgtg | 1680 |
| gcagaagtga | atccaccggc | tccccgggtc | aaagcgctct | gggtccataa | aacgggctct | 1740 |
| actggcgggt | ttggcagcta | cgtggccttt | attcctgaaa | agcagatcgg | tattgtgatg | 1800 |
| ctcgcgaata | caagctatcc | gaaccgggca | cgcgttgagg | cggcatacca | tatcctcgag | 1860 |
| gcgctacag | | | | | | 1869 |

<210> 5
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB 1.11 construct

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Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
20 25 30
Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
50 55 60
Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Asp
65 70 75 80
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
130 135 140
Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys
145 150 155 160
Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
165 170 175
Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
180 185 190
Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
195 200 205
Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
210 215 220
Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225 230 235 240
Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
245 250 255
Ser Val Thr Val Ser Ser
260

<210> 6
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> CAB 1.11 construct

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atgtcctgca gagcgggtga gtctgttgac attttcggtg tcggttttct gcaactggtac 120
caacagaaac cgggtcagcc gccaaaactg ctgatctatc gtgcttctaa cctggagtcc 180
ggcatcccggtacgtttctc cgggtactggc tctgggtactg attttaccct gattatcgac 240


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ccggtggaag cagacgatgt tgccacctac tattgccage agaccaacga ggatccgtac 300
accttcggtg gcggtactaa actggagatc aaaggcggtg gtggttctgg tgggtggtgt 360
agcgggtggcg gtggtagcgg tggcggtggc agcggtggtg gtggtctctgg tggcggtggc 420
tctgaagtgc agctgcagca gtccggtgcg gagctcgttg aaccgggcgc ttctgtgaaa 480
ctgtcttgca ctgcattctgg tttcaacatt aaggacacct acatgcactg ggtgaaacaa 540
cgcccggaac aggggtctgga gtggatcggg cgcattcgatc cggctaacgg taacagcaaa 600
tacgtgccaa aattccaggg taaagcaacc atcactgctg atacctcctc taacactgct 660
tacctgcagc tgacttcctt gactagcgaa gacaccggcg tttattactg cgctccgttc 720
ggctactatg tcagcgatta cgcaatggcc tactgggggtc agggcacctc tgttaccgtt 780
tctagc 786

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<210> 7
<211> 623
<212> PRT
<213> Artificial Sequence

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<220>
<223> CAB 1.11 construct

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<400> 7
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Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
20        25        30
Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35        40        45
Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
50        55        60
Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Asp
65        70        75        80
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
85        90        95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100       105       110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115       120       125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
130       135       140
Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys
145       150       155       160
Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
165       170       175
Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
180       185       190
Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
195       200       205
Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
210       215       220
Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225       230       235       240
Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
245       250       255
Ser Val Thr Val Ser Ser Thr Pro Val Ser Glu Lys Gln Leu Ala Glu
260       265       270
Val Val Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro
275       280       285
Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr

```

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|--|
| | 290 | | | | | 295 | | | | | | 300 | | | | | | | |
| Phe | Gly | Lys | Ala | Asp | Ile | Ala | Ala | Asn | Lys | Pro | Val | Thr | Pro | Gln | Thr | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | | | | 320 | |
| Leu | Phe | Glu | Leu | Gly | Ser | Ile | Ser | Lys | Thr | Phe | Thr | Gly | Val | L | | | | | |